

G. Kovalenko

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RAW SEQUENCE LISTING

DATE: 07/12/2000

PATENT APPLICATION: US/09/380,546

TIME: 13:46:00

Input Set : A:\Wall123.app

Output Set: N:\CRF3\07122000\I380546.raw

3 <110> APPLICANT: WALLACH, David
4 GOLTSEV, Yura
5 KOVALENKO, Andrei
6 VARFOLOMEEV, Eugene
7 BRODIANSKI, Vadim
9 <120> TITLE OF INVENTION: CASH (CASPASE HOMOLOGUE) WITH DEATH EFFECTOR DOMAIN,
10 MODULATORS OF THE FUNCTION OF FAS RECEPTORS
12 <130> FILE REFERENCE: WALLACH=23
14 <140> CURRENT APPLICATION NUMBER: 09/380,546
15 <141> CURRENT FILING DATE: 1999-11-29
17 <150> PRIOR APPLICATION NUMBER: PCT/IL98/00098
18 <151> PRIOR FILING DATE: 1998-02-26
20 <150> PRIOR APPLICATION NUMBER: IL 120367
21 <151> PRIOR FILING DATE: 1997-03-03
23 <150> PRIOR APPLICATION NUMBER: IL120759
24 <151> PRIOR FILING DATE: 1997-05-01
26 <160> NUMBER OF SEQ ID NOS: 22
28 <170> SOFTWARE: PatentIn Ver. 2.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 2243
32 <212> TYPE: DNA
33 <213> ORGANISM: Homo sapiens
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37 ctacccgacg agtctcaact aaaagggact cccggagcta ggggtgggga ctccggcctca 120
38 cacagtgaat gccggctatt ggacttttgt ccagtgcagc ctgagacaac aaggaccacg 180
39 ggaggagggtg taggagagaa gcgcgcgcaa cagcgatcgc ccagcaccaa gtccgcttcc 240
40 aggccttctcg tttctttgcc tccatcttgg gtgcgccttc ccggcgctca ggggagcgaa 300
41 ggctgagggtg gcagcggcag gagagtcggc ccgcgacagg acgaactccc ccaactggaa 360
42 ggattctgaa agaaatgaag tcagccctca gaaatgaagt tgactgcctg ctggccttcc 420
43 tgttgactgg cccggagctg tactgcaaga cccttgtgag ctccctagat ctaagagtag 480
44 gatgtctgct gaagtcaccc atcaggttga agaagcactt gatacagatg agaaggagat 540
45 gctgctcttt ttgtgccggg atgttgctat agatgtgggt ccacctaatg tcagggacct 600
46 tctggatatt ttacgggaaa gaggtaagct gtctgtcggg gacttgctg aactgctcta 660
47 cagagtgaag cgatttgacc tgcctaaaac tatcttgaag atggacagaa aagctgtgga 720
48 gacccacctg ctacaggaacc ctacacttgt ttcggactat agagtgtgta tggcagagat 780
49 tggtaggat ttggataaat ctgatgtgtc ctcatataat ttctcatga aggtattacat 840
50 gggccgagga aagataagca aggagaagag tttcttggac ctgtgtggtg agttggagaa 900
51 actaaatttg gttgccccag atcaactgga tttattagaa aaatgcctaa agaactcca 960
52 cagaatagac ctgaagacaa aaatccagaa gtacaagcag tctgttcaag gagcagggac 1020
53 aagttacagg aatgttctcc aagcagcaat ccaaaagagt ctcaaggatc cttcaataaa 1080
54 ctccaggctc cataatggga gaagtaaaga acaaaagactt aaggaaacagc ttggcgctca 1140
55 acaagaacca gtgaagaaat ccattcagga atcagaagct tttttgcctc agagcatacc 1200
56 tgaagagaga tacaagatga agagcaagcc cctaggaatc tgcctgataa tcgattgcat 1260
57 tggcaatgag acagagcttc ttcgagacac ctccacttcc ctgggctatg aagtcagaaa 1320
58 attcttgcac ctacgtatgc atgttatatc ccagattctt ggccaatttg cctgtatgcc 1380
59 cgagcaccga gactacgaca gctttgtgtg tgtcctgggt agccgaggag gctcccagag 1440

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60 tgtgtatggt gtggatcaga ctcaactcagg gctccccctg catcacatca ggaggatgtt 1500
61 catggggagat tcatgccctt atctagcagg gaagccaaag atgtttttta ttcagaacta 1560
62 tgtgggtgtca gagggccagc tggagaacag cagcctcttg gaggtggatg ggccagcgat 1620
63 gaagaatgtg gaattcaagg ctcaagaagc agggctgtgc acagttcacc gagaagctga 1680
64 cttcttcttg agcctgtgta ctgcggacat gtccctgctg gagcagtcct acagctcacc 1740
65 gtccctgtac ctgcagtgcc tctcccagaa actgagacaa gaaagaaaac gcccaactcct 1800
66 ggatcttcac attgaactca atggctacat gtatgattgg aacagcagag tttctgccaa 1860
67 ggagaaatat tatgtctggc tgcagcacac tctgagaaag aaacttatcc tctcctacac 1920
68 ataagaaacc aaaaggctgg gcgtagtggc tcacacctgt aatcccagca ctttgggagg 1980
69 ccaaggaggg cagatcaact caggtcagga gtctgagacc agcctggcca acatggtaaa 2040
70 cgctgtccct agtaaaaaatg caaaaattag ctgggtgtgg gtgtgggtac ctgtgttccc 2100
71 agttacttgg gaggtgagg tgggaggatc ttttgaacct aggagttcag ggtcatagca 2160
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82 1 5 10 15
84 Glu Lys Glu Met Leu Leu Phe Leu Cys Arg Asp Val Ala Ile Asp Val
85 20 25 30
87 Val Pro Pro Asn Val Arg Asp Leu Leu Asp Ile Leu Arg Glu Arg Gly
88 35 40 45
90 Lys Leu Ser Val Gly Asp Leu Ala Glu Leu Leu Tyr Arg Val Arg Arg
91 50 55 60
93 Phe Asp Leu Leu Lys Arg Ile Leu Lys Met Asp Arg Lys Ala Val Glu
94 65 70 75 80
96 Thr His Leu Leu Asn Pro His Leu Val Ser Asp Tyr Arg Val Leu Met
97 85 90 95
99 Ala Glu Ile Gly Glu Asp Leu Asp Lys Ser Asp Val Ser Ser Leu Ile
100 100 105 110
102 Phe Leu Met Lys Asp Tyr Met Gly Arg Gly Lys Ile Ser Lys Glu Lys
103 115 120 125
105 Ser Phe Leu Asp Leu Val Val Glu Leu Glu Lys Leu Asn Leu Val Ala
106 130 135 140
108 Pro Asp Gln Leu Asp Leu Leu Glu Lys Cys Leu Lys Asn Ile His Arg
109 145 150 155 160
111 Ile Asp Leu Lys Thr Lys Ile Gln Lys Tyr Lys Gln Ser Val Gln Gly
112 165 170 175
114 Ala Gly Thr Ser Tyr Arg Asn Val Leu Gln Ala Ala Ile Gln Lys Ser
115 180 185 190
117 Leu Lys Asp Pro Ser Asn Asn Phe Arg Leu His Asn Gly Arg Ser Lys
118 195 200 205
120 Glu Gln Arg Leu Lys Glu Gln Leu Gly Ala Gln Gln Glu Pro Val Lys
121 210 215 220
123 Lys Ser Ile Gln Glu Ser Glu Ala Phe Leu Pro Gln Ser Ile Pro Glu
124 225 230 235 240

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126 Glu Arg Tyr Lys Met Lys Ser Lys Pro Leu Gly Ile Cys Leu Ile Ile
127      245      250      255
129 Asp Cys Ile Gly Asn Glu Thr Glu Leu Leu Arg Asp Thr Phe Thr Ser
130      260      265      270
132 Leu Gly Tyr Glu Val Gln Lys Phe Leu His Leu Ser Met His Gly Ile
133      275      280      285
135 Ser Gln Ile Leu Gly Gln Phe Ala Cys Met Pro Glu His Arg Asp Tyr
136      290      295      300
138 Asp Ser Phe Val Cys Val Leu Val Ser Arg Gly Gly Ser Gln Ser Val
139 305      310      315      320
141 Tyr Gly Val Asp Gln Thr His Ser Gly Leu Pro Leu His His Ile Arg
142      325      330      335
144 Arg Met Phe Met Gly Asp Ser Cys Pro Tyr Leu Ala Gly Lys Pro Lys
145      340      345      350
147 Met Phe Phe Ile Gln Asn Tyr Val Val Ser Glu Gly Gln Leu Glu Asn
148      355      360      365
150 Ser Ser Leu Leu Glu Val Asp Gly Pro Ala Met Lys Asn Val Glu Phe
151      370      375      380
153 Lys Ala Gln Lys Arg Gly Leu Cys Thr Val His Arg Glu Ala Asp Phe
154 385      390      395      400
156 Phe Trp Ser Leu Cys Thr Ala Asp Met Ser Leu Leu Glu Gln Ser His
157      405      410      415
159 Ser Ser Pro Ser Leu Tyr Leu Gln Cys Leu Ser Gln Lys Leu Arg Gln
160      420      425      430
162 Glu Arg Lys Arg Pro Leu Leu Asp Leu His Ile Glu Leu Asn Gly Tyr
163      435      440      445
165 Met Tyr Asp Trp Asn Ser Arg Val Ser Ala Lys Glu Lys Tyr Tyr Val
166      450      455      460
168 Trp Leu Gln His Thr Leu Arg Lys Lys Leu Ile Leu Ser Tyr Thr Glx
169 465      470      475      480
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176 <211> LENGTH: 1373
177 <212> TYPE: DNA
178 <213> ORGANISM: Homo sapiens
180 <400> SEQUENCE: 3
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182 ctcaccgacg agtctcaact aaaagggact cccggagcta ggggtgggga ctccggcctca 120
183 cacagtgaag gccggctatt ggacttttgt ccagtgcacg ctgagacaac aaggaccacg 180
184 ggaggagggt taggagagaa gcgcgcgcaa cagcgatcgc ccagcaccaa gtccgcttcc 240
185 aggcctttcg tttctttgcc tccatcttgg gtgcgccttc ccggcgctca ggggagcgaa 300
186 ggctgagggt gcagcggcag gagagtccgg ccgcgacagg acgaactccc cactgggaaa 360
187 ggattctgaa agaaatgaag tcagccctca gaaatgaagt tgactgcctg ctggctttcc 420
188 tgttgactgg cccggagctg tactgcaaga cccttgtagg ctccctagt ctaagagtag 480
189 gatgtctgct gaagtcattc atcaggttga agaagcactt gatacagatg agaaggagat 540
190 gctgtctttt ttgtgcggg atgttgctat agatgtggtt ccacctaatg tcaggacact 600
191 tctggatatt ttacgggaaa gaggtaaagt gtctgtcggg gacttggtg aactgctcta 660
192 cagagtgaag cgatttgacc tgctcaaacg tatcttgaag atggacagaa aagctgtgga 720
193 gaccacactg ctcaggaaac ctcacctgtg ttcggactat agagtgtgta tggcagagat 780
194 tggtgaggat ttggataaat ctgatgtgtc ctcattaatt ttctcatga aggattacat 840

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195 gggccgaggc aagataagca aggagaagag tttcttggac cttgtggttg agttggagaa 900
196 actaaatttg gttgccccag atcaactgga tttattagaa aaatgcctaa agaacaatcca 960
197 cagaatagac ctgaagacaa aaatccagaa gtacaagcag tctgttcaag gagcagggac 1020
198 aagttacagg aatgttctcc aagcagcaat ccaaaagagt ctcaaggatc cttcaaataa 1080
199 cttcaggatg ataacaccct atgcccattg tcctgatctg aaaattcttg gaaattgttc 1140
200 catgtgatta acatggaact gcctctactt aatcattctg aatgattaaa tcgtttcatt 1200
201 ttctaaatgt gttataatgt gtttagccct ttcttgttgc tgtatgttta gatgctttcc 1260
202 aatcttttgt tactactaat aatgctataa aataaatatc cttgtacttc ttaaaaaaaaa 1320
203 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1373

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205 <210> SEQ ID NO: 4
206 <211> LENGTH: 222
207 <212> TYPE: PRT
208 <213> ORGANISM: Homo sapiens
210 <400> SEQUENCE: 4
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212 1 5 10 15
214 Glu Lys Glu Met Leu Leu Phe Leu Cys Arg Asp Val Ala Ile Asp Val
215 20 25 30
217 Val Pro Pro Asn Val Arg Asp Leu Leu Asp Ile Leu Arg Glu Arg Gly
218 35 40 45
220 Lys Leu Ser Val Gly Asp Leu Ala Glu Leu Leu Tyr Arg Val Arg Arg
221 50 55 60
223 Phe Asp Leu Leu Lys Arg Ile Leu Lys Met Asp Arg Lys Ala Val Glu
224 65 70 75 80
226 Thr His Leu Leu Arg Asn Pro His Leu Val Ser Asp Tyr Arg Val Leu
227 85 90 95
229 Met Ala Glu Ile Gly Glu Asp Leu Asp Lys Ser Asp Val Ser Ser Leu
230 100 105 110
232 Ile Phe Leu Met Lys Asp Tyr Met Gly Arg Gly Lys Ile Ser Lys Glu
233 115 120 125
235 Lys Ser Phe Leu Asp Leu Val Val Glu Leu Glu Lys Leu Asn Leu Val
236 130 135 140
238 Ala Pro Asp Gln Leu Asp Leu Leu Glu Lys Cys Leu Lys Asn Ile His
239 145 150 155 160
241 Arg Ile Asp Leu Lys Thr Lys Ile Gln Lys Tyr Lys Gln Ser Val Gln
242 165 170 175
244 Gly Ala Gly Thr Ser Tyr Arg Asn Val Leu Gln Ala Ala Ile Gln Lys
245 180 185 190
247 Ser Leu Lys Asp Pro Ser Asn Asn Phe Arg Met Ile Thr Pro Tyr Ala
248 195 200 205
250 His Cys Pro Asp Leu Lys Ile Leu Gly Asn Cys Ser Met Glx
251 210 215 220

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254 <210> SEQ ID NO: 5
255 <211> LENGTH: 484
256 <212> TYPE: PRT
257 <213> ORGANISM: Mus musculus
259 <400> SEQUENCE: 5
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263 Cys Leu Asp Glu Asp Glu Lys Glu Met Met Leu Phe Leu Cys Arg Asp
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266 Val Thr Glu Asn Leu Ala Ala Pro Asn Val Arg Asp Leu Leu Asp Ser
267          35          40          45
269 Leu Ser Glu Arg Gly Gln Leu Ser Phe Ala Thr Leu Ala Glu Leu Leu
270          50          55          60
272 Tyr Arg Val Arg Arg Phe Asp Leu Leu Lys Arg Ile Leu Lys Thr Asp
273 65          70          75          80
275 Lys Ala Thr Val Glu Asp His Leu Arg Arg Asn Pro His Leu Val Ser
276          85          90          95
278 Asp Tyr Arg Val Leu Leu Met Glu Ile Gly Glu Ser Leu Asp Gln Asn
279          100         105         110
281 Asp Val Ser Ser Leu Val Phe Leu Thr Arg Ile Thr Arg Asp Tyr Thr
282          115         120         125
284 Gly Arg Gly Lys Ile Ala Lys Asp Lys Ser Phe Leu Asp Leu Val Ile
285          130         135         140
287 Glu Leu Glu Lys Leu Asn Leu Ile Ala Ser Asp Gln Leu Asn Leu Leu
288 145         150         155         160
290 Glu Lys Cys Leu Lys Asn Ile His Arg Ile Asp Leu Asn Thr Lys Ile
291          165         170         175
293 Gln Lys Tyr Thr Gln Ser Ser Gln Gly Ala Arg Ser Asn Met Asn Thr
294          180         185         190
296 Leu Gln Ala Ser Leu Pro Lys Leu Ser Ile Lys Tyr Asn Ser Arg Leu
297          195         200         205
299 Gln Asn Gly Arg Ser Lys Glu Pro Arg Phe Val Glu Tyr Arg Asp Ser
300          210         215         220
302 Gln Arg Thr Leu Val Lys Thr Ser Ile Gln Glu Ser Gly Ala Phe Leu
303 225         230         235         240
305 Pro Pro His Ile Arg Glu Glu Thr Tyr Arg Met Gln Ser Lys Pro Leu
306          245         250         255
308 Gly Ile Cys Leu Ile Ile Asp Cys Ile Gly Asn Asp Thr Lys Tyr Leu
309          260         265         270
311 Gln Glu Thr Phe Thr Ser Leu Gly Tyr His Ile Gln Leu Phe Leu Phe
312          275         280         285
314 Pro Lys Ser His Asp Ile Thr Gln Ile Val Arg Arg Tyr Ala Ser Met
315          290         295         300
317 Ala Gln His Gln Asp Tyr Asp Ser Phe Ala Cys Val Leu Val Ser Leu
318 305         310         315         320
320 Gly Gly Ser Gln Ser Met Met Gly Arg Asp Gln Val His Ser Gly Phe
321          325         330         335
323 Ser Leu Asp His Val Lys Asn Met Phe Thr Gly Asp Thr Cys Pro Ser
324          340         345         350
326 Leu Arg Gly Lys Pro Lys Leu Phe Phe Ile Gln Asn Tyr Glu Ser Leu
327          355         360         365
329 Gly Ser Gln Leu Glu Asp Ser Ser Leu Glu Val Asp Gly Pro Ser Ile
330          370         375         380
332 Lys Asn Val Asp Ser Lys Pro Leu Gln Pro Arg His Cys Thr Thr His
333 385         390         395         400
335 Pro Glu Ala Asp Ile Phe Trp Ser Leu Cys Thr Ala Asp Val Ser His

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